

- <110> WALLACH, David BolDIN, Mark MALININ, Nikolai
- <120 MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS
- <130 WALLACH24</pre>
- $\pm (140 \pm 0)^{\circ}$
- +:141 × 1999-12-06
- +1150 + 1.11011 +1151 + 1.497-06-05
- $\pm 0.150 \pm 1.11199$
- +.151 + 1497-06-30
- 1150 × 111746 1151 × 1197-09-11
- $\pm 160 \pm 2$
- -: 170 · PatentIn Ver. 2.0
- H210 1
- -0911 540
- +1.212 + PF.T
- +3313 Homo sapiens
- +:400.+ 1
- Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
- Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
- Sor Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
- Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
- Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro
- The Leu Gly lie Cys Ash Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
- Tyr Met Pro Asr. Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
- Tyr Pro Asp Mal Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile 120
- Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His



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His 145	Asp	Leu	Lys	Thr	31n 150	Asn	Ile	Leu	Leu	Asp 155	Asn	Glu	Phe	His	Val 160
Lys	lle	Ala	Asp	Phe 165	317	Leu	Ser	Lys	Trp 170	Arg	Met	Met	Ser	Leu 175	Ser
Gln	Ser	Arg	Ser 130	Ser	Lys	Ser	Ala	Pro 185	Gl:	Gly	Gly	Thr	Ile 190	Ile	Tyr
Met	Pro	Pro 195	ЗLы	Asn	Tyr	Эlu	Pro 201	Gly	Gla	Lys	Ser	Arg 2)5	Alā	Ser	Ile
Lys	His 210	Asp	He	Туг	Ser	Tyr 215	Ala	Val.	Ile	Thr	Frp 220	31u	Val	Leu	Ser
Ang 215	ГАЗ	Gln	Pro	Phe	Glu 230	Asp	Val	Thr	Asn	Pro 235	Leu	Gin	Ile	Met.	Tyr 240
Ser	Val	Ser	Glr	GLy 245	His	Arg	Pro	Val	Ile 250	Asn	Glu	Glu	Ser	Leu 255	Pro
T;r	Asp	Il∈	Pro 260	His	Arg	Ala	Arg	:Met :265	Ilə	Ser	Leu	Ile	Glu 270	Ser	GLY
Trp	Alla	Gln 275	Aar.	Pro	Asp	Glu	Arg 280	Pro	Ser	Ph∈	Leu	Lys 285	Суг	Leu	I.ê
Glu	Leu 290	Gl.	Pri	Val.	Leu	Arg 295	Thr	Phe	Glu	31u	Ile 300	Thr	Ph∈	Leu	Glu
Ala 305	Va !	Tle	E -	7.€0	313	, · · · . d	ሞኮ ∽	* 7°	" <u>a</u>	315	Sar	·7.4 1	Ser	Ser	.01.a 3.10
Tle	Him	Let	Cys	Asp 325	Tys	Lys	Lys	Met	Glu 330	Leu	Ser	Lou	Asn	11c 333	250
Val	Asn	His	Gly 341	Pro	Glm	Glu	Glu	3er 345	Суз	Gly	Ser	3er	Gln 350	Leu	Hls
Glu	Asn	Ser 353	G.y	S∈r	Pro	Glu	Thr 360	Ser	Arq	Ser	Leu	Pro 365	Ala	Pro	Gliri
Asp	Asn 370	Asp	Pho	Per	Ser	Arg 375	Lys	Ala	Glr.	Asp	Cys 380	Tyr	Phe	Иеt.	Lys
Leu 385	His	His	Cys	Pro	G17 390	Asr.	His	B⊜r	Trp	Asp 395	Ser	Thr	Ile	Ser	G.5 400
Ser	Glr.	Arg	Ala	Ala 405	Phe	Cys	Asp	His	Туа 410	Thr	Thr	Pro	Cys	S∈r 415	Ser
Ala	Ile	Ile	Asn 420	Pro	Leu	Ser	Thr	Ala 425	Gly	Asn.	Ser	Gla	Arg 430	Leu	Glr.
Pro	Gly	11e 435	Ala	GIE.	Gin	Trp	T ! ↔ 4 4 0	(3) n	Ser	i.ys	Arg	G_u 445	Asp	Ile	Vall
Asn	Gln 450	Меt	Thr	Glu	Ala	Cys 455	Leu	Asn	Gln	Ser	Leu 460	qзА	Ala	Leu	Leu
Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Āsp	Tyr	Glu	Leu	Val	Ser	Thr	Lys

465 475 475

Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp IIe 485 490 490

Grn Gly Glu Glu Phe Ala Lys Val Tie Val Gln Lys Leu Lys Asp Asn 500 500

Lys Gin Mot Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg 515 520 525

Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met 530 540

<2105 €

NETIC 2098

4212+ DNA

CD13 - Homo sapiens

 $\pm 400 \times 2$

quodattatg gatggatggg oggogotacg gogttggcab dagtototag aaaagaagtb 🙉 ugototgytt bygagaagda gogyptygog tyggobatbo gyggaatygg ogobotogty $1.0\,$ rootageget geggggeaaa aagggteteg eeggeetege tegegeaggg gegtatetgg 1-0gagodtjago goggogtiggg agoottiggga googoogbag cajjigggdac accoggaabo .40 qqortgagog obogggadda tgaaqqggga qqobatotgo agogdootgo boaddattoo (80) stabbabaaa etegeogabb tqeqotaeet qaqboqqqq qobtotqqba otqtqtqtbqtb 360 sycongenae geagaetgge gegteeaggt gyengtyaay nachtghaca tehaeaetee $4.0\,$ ${\it potgotogae}$ agtgaaagaa aggatgtttt aagagaagot gaaattttac acaaagotag 4%unstagorad accomposaa ottogggaat otgbaatgag Soogaatoot ogggaalwyb 840 habbqaatad abgobaaabg gabbabbaaa bgaabbobba babaggaaaa bbgaababbb 600 ndatyttyst tyyddannga yannhogoar obrynanyaa athybbsty ytytaaatta 🕬 ostgoadaat atgastooto Stitaotisa toatgastig aagastoaga atatsitati quadaatgaa ottoatgtoa agattgdaga tittiggtota toaaagtggo goatgatgto perferenced transpalagra gradatirtgo appagaagga gggabaatta titatatgob Amotyaaaad tatgaaboty gadaaaaato aaggybbagt atbaagbaby atatatatag 🕮 onacycaget accapacygy asytythato caysaasabay dottetysay acythabbas 400 tootttypag ataatytata ytytytoaba ayyabatoya botyttatta atgaayaaay $1\,\%0$ integocatat gatababeto abogagidaog tatgatotot otaatagaaa geggatgggo 1.54 kisaaaatoba gatgaaagab batottoott aaaatgtota atagaabtig aabbagtott gagaacatti gaagagataa ottitootiga ayotgitati cagotaaaga aaacaaagti adagagtigtt toaagtigooa bibabotatig tigabaagaag aaaatiggaat tabototigaa 1160 catabotyta aatoatygtu babaagagya abbatytyya toototbayo tobatyaasa 1920 taginguist congagaett caaggiooot googotoot caagacaatg attititato tagaaaagot baagabtgit attitatgaa gotgoatbab tgtootggaa atbabagitig [440 gratageade attititiggat oteaaargge typattetyt gateadaaga beadtedatg ototicagea asaataaato babtotoaac tybaggaaab toagaabyto tybagbotgg tatagoccag dagtggatoc agagoaaaaag ggaagacatt gtgaaccaaa tgacagaago 1.20 ongostraad dagtogotag atgodottot gtobagggab ttgalbatga aagaggabta tqaabttgtt aqtabbaaqb otabaaqgab otbaaaaagtb agabaattab tagababtab tqacatcbaa qqaqaagaat ttgbbaaaagt tatagtabaa aaattgaaag ataabaaaca antgggtott cagoottabo oggaaatabt tgtggtttbt agatbabbat btttaaattt acticamaat mamagisityi magigaciyi titticaagaa qamatyijit teatamaagy 1930 arattiatat ototigitigot etgaptittit tiatataaaa toogegagta tiaaaagettw 1953 awwraargkt cittarktaa atattagtot cootcoatga cactgoagta tittiittaa 19040 ttaatacaag taaaaagttg aatttgaaaa наняяняаан аааааааааа аааазааа -2Jhoo

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
 - (B) STREET: WEIZMANN INSTITUTE OF SCIENCE, P.O.B. 95
 - (C) CITY: REHOVOT
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 - (C) CITY: REHOVOT
 - (E) COUNTRY: ISRAEL
 - (F) POSTAL CODE (ZIP): 76406
 - (A) NAME: BOLDIN, MARK
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 - (C) CITY: REHOVOT
 - (E) COUNTRY: ISRAEL
 - (F) POSTAL CODE (ZIP): 76100
 - (A) NAME: MALININ, NIKOLAI
 - (B) STREET: BEIT CLOFE, WEIZMANN INSTITUTE OF SCIENCE
 - (C) CITY: REHOVOT
 - (E) COUNTRY: ISRAEL
 - (F) POSTAL CODE (ZIP): 76100
- (ii) TITLE OF INVENTION: MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 121011
 - (B) FILING DATE: 05-JUN-1997
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 121199
 - (B) FILING DATE: 30-JUN-1997
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 121746
 - (B) FILING DATE: 11-SEP-1997
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDM: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His 1 5 10 15

Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val $\frac{20}{100}$

Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
35 40 45

Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu 50 60

Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro 65 70 75 80

Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu 85 90 95

Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu 100 105 110

Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile 115 120 125

Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His 130 140

His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val 145 150 155 160

Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser 165 170 175

Gin Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr 180 185 190

Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile 195 200 205

Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser

Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr 225 230 235 240

Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro 245 250 255

Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly 260 265 270

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'Trp Ala Gln Asn Plass Glu Arg Pro Ser Phe Leu Lys Cylleu Ile Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu 295 Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala Ile His Leu Cys Asp Lys Lys Met Glu Leu Ser Leu Asn Ile Pro Val Asn His Gly Pro Gla Glu Glu Ser Cys Gly Ser Ser Gla Leu His 345 340 Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln 360 Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys 375 380 Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys 475 470 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile 485 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn 505 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met 535

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2098 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGCCATTATG	GATGGATGGG	CGGCGCTACG	GCGTTGGCAC	CAGTCTCTAG	AAAAGAAGTC	6 0
AGCTCTGGTT	CGGAGAAGCA	GCGGCTGGCG	TGGGCCATCC	GGGGAATGGG	CGCCCTCGTG	120
ACCTAGTGTT	GCGGGGCAAA	AAGGGTCTTG	CCGGCCTCGC	TEGTGCAGGG	GCGTATCTGG	130
GCGCCTGAGC	GCGGCGTGGG	AGCCTTGGGA	GCCGCCGCAG	CAGGGGGCAC	ACCCGGAACC	240
GGCCTGAGCG	CCCGGGACCA	TGAACGGGGA	GGCCATCTGC	AGCGCCCTGC	CCACCATTCC	300
CTACCACAAA	CTCGCCGACC	TGCGCTACCT	GAGCCGCGGC	GCCTCTGGCA	CTGTGTCGTC	360
CGCCCGCCAC	GCAGACTGGC	GCGTCCAGGT	GGCCGTGAAG	CACCTGCACA	TCCACACTCC	420
GCTGCTCGAC	AGTGAAAGAA	AGGATGTTTT	AAGAGAAGCT	GAAATTTTAC	ACAAAGCTAG	430
ATTTAGTTAC	ATTTTTCCAA	TTTTGGGAAT	TTGCAATGAG	CCTGAATTTT	TGGGAATAGT	540
TACTGAATAC	ATGCCAAATG	GATCATTAAA	TGAACTCCTA	CATAGGAAAA	CTGAATATCC	600
TGATGTTGCT	TGGCCATTGA	GATTTCGCAT	CCTGCATGAA	ATTGCCCTTG	GTGTAAATTA	6 60
CCTGCACAAT	ATGACTCCTC	CTTTACTTCA	TCATGACTTG	AAGACTCAGA	ATATCTTATT	720
GGACAATGAA	TTTCATGTTA	AGATTGCAGA	TTTTGGTTTA	TCAAAGTGGC	GCATGATGTC	780
CCTCTCACAG	TCACGAAGTA	GCAAATCTGC	ACCAGAAGGA	GGGACAATTA	TTTATATGCC	840
ACCTGAAAAC	TATGAACCTG	GACAAAAATC	AAGGGCCAGT	ATCAAGCACG	ATATATATAG	900
CTATGCAGTT	ATCACATGGG	AAGTGTTATC	CAGAAAACAG	CCTTTTGAAG	ATGTCACCAA	960
TCCTTTGCAG	ATAATGTATA	GTGTGTCACA	GAAGCATCGA	CCTGTTATTA	ATGAAGAAAG	1020
TTTGCCATAT	GATATACCTC	ACCGAGCACG	TATGATCTCT	CTAATAGAAA	GTGGATGGGC	1080
ACAAAATCCA	GATGAAAGAC	CATCTTTCTT	AAAATGTTTA	ATAGAACTTG	AACCAGTTTT	1140
GAGAACATTT	GAAGAGATAA	CTTTTCTTGA	AGCTGTTATT	CAGCTAAAGA	AAACAAAGTT	1200
ACAGAGTGTT	TCAAGTGCCA	TTCACCTATG	TGACAAGAAG	AAAATGGAAT	TATCTCTGAA	1260
CATACCTGTA	AATCATGGTC	CACAAGAGGA	ATCATGTGGA	TCCTCTCAGC	TCCATGAAAA	1320
TAGTGGTTCT	CCTGAAACTT	CAAGGTCCCT	GCCAGCTCCT	CAAGACAATG	ATTTTTTATC	1380
TAGAAAAGCT	CAAGACTGTT	ATTTTATGAA	GCTGCATCAC	TGTCCTGGAA	ATCACAGTTG	1440
GGATAGCACC	ATTICTGGAT	CTCAAAGGGC	TGCATTCTGT	GATCACAAGA	CCACTCCATG	1500
CTCTTCAGCA	ATAATAAATC	CACTCTCAAC	TGCAGGAAAC	TCAGAACGTC	TGCAGCCTGG	1550
TATAGCCCAG	CAGTGGATCC	AGAGCAAAAG	GGAAGACATT	GTGAACCAAA	TGACAGAAGC	1620
CTGCCTTAAC	CAGTCGCTAG	ATGCCCTTCT	GTCCAGGGAC	TTGATCATGA	AAGAGGACTA	1680

TGAACTTGTT	AGTACCAAGC	AAGGAC	CTCAAAAGTC	AGACAATTAC	TAG. CTAC	1740
TGACATCCAA	GGAGAAGAAT	TTGCCAAAGT	TATAGTACAA	AAATTGAAAG	ATAACAAACA	1800
AATGGGTCTT	CAGCCTTACC	CGGAAATACT	TGTGGTTTCT	AGATCACCAT	CTTTAAATTT	1860 ;
ACTTCAAAAT	AAAAGCATGT	AAGTGACTGT	TTTTCAAGAA	GAAATGTGTT	TCATAAAAGG	1920
ATATTTATAT	CTCTGTTGCT	TTGACTTTTT	TTATATAAAA	TCCGTGAGTA	TTAAAGCTTW	1980
AWWRAARGKT	CTTTSRKTAA	ATATTAGTCT	CCCTCCATGA	CACTGCAGTA	TTTTTTTAA	2040
TTAATACAAG	TAAAAAGTTG	AATTTGAAAA.	ААААААААА	AAAAAAAAA	AAAAAAA	2098

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